SEQUENCE LISTING

<110> Adeokun, Anthonia Monisola
        Ambrose, Helen
        Cresswell, Carl
        Dudley, Adam

<120> Chemical Compounds

<130> 06275-264002

<140> US 10/698,808
<141> 2003-10-31

<150> US 09/925,731
<151> 2001-08-10

<150> US 60/226,909
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                                            Met Asp Gln Asn Gln
                                             1               5

cat ttg aat aaa aca gca gag gca caa cct tca gag aat aag aaa aca       162
His Leu Asn Lys Thr Ala Glu Ala Gln Pro Ser Glu Asn Lys Lys Thr
            10                  15                  20

aga tac tgc aat gga ttg aag atg ttc ttg gca gct ctg tca ctc agc       210
Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala Ala Leu Ser Leu Ser
            25                  30                  35

ttt att gct aag aca cta ggt gca att att atg aaa agt tcc atc att       258
Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met Lys Ser Ser Ile Ile
            40                  45                  50

cat ata gaa cgg aga ttt gag ata tcc tct tct ctt gtt ggt ttt att       306
His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser Leu Val Gly Phe Ile
    55                  60                  65
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gac gga agc ttt gaa att gga aat ttg ctt gtg att gta ttt gtg agt        354
Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val Ile Val Phe Val Ser
 70              75              80              85

tac ttt gga tcc aaa cta cat aga cca aag tta att gga atc ggt tgt        402
Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu Ile Gly Ile Gly Cys
             90              95             100

ttc att atg gga att gga ggt gtt ttg act gct ttg cca cat ttc ttc        450
Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala Leu Pro His Phe Phe
            105             110             115

atg gga tat tac agg tat tct aaa gaa act aat atc aat tca tca gaa        498
Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn Ile Asn Ser Ser Glu
            120             125             130

aat tca aca tcg acc tta tcc act tgt tta att aat caa att tta tca        546
Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile Asn Gln Ile Leu Ser
            135             140             145

ctc aat aga gca tca cct gag ata gtg gga aaa ggt tgt tta aag gaa        594
Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys Gly Cys Leu Lys Glu
150             155             160             165

tct ggg tca tac atg tgg ata tat gtg ttc atg ggt aat atg ctt cgt        642
Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met Gly Asn Met Leu Arg
            170             175             180

gga ata ggg gag act ccc ata gta cca ctg ggg ctt tct tac att gat        690
Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly Leu Ser Tyr Ile Asp
            185             190             195

gat ttc gct aaa gaa gga cat tct tct ttg tat tta ggt ata ttg aat        738
Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr Leu Gly Ile Leu Asn
            200             205             210

gca ata gca atg att ggt cca atc att ggc ttt acc ctg gga tct ctg        786
Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe Thr Leu Gly Ser Leu
            215             220             225

ttt tct aaa atg tac gtg gat att gga tat gta gat cta agc act atc        834
Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val Asp Leu Ser Thr Ile
230             235             240             245

agg ata act cct act gat tct cga tgg gtt gga gct tgg tgg ctt aat        882
Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly Ala Trp Trp Leu Asn
            250             255             260

ttc ctt gtg tct gga cta ttc tcc att att tct tcc ata cca ttc ttt        930
Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser Ser Ile Pro Phe Phe
            265             270             275

ttc ttg ccc caa act cca aat aaa cca caa aaa gaa aga aaa gct tca        978
Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys Glu Arg Lys Ala Ser
            280             285             290
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ctg tct ttg cat gtg ctg gaa aca aat gat gaa aag gat caa aca gct     1026
Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu Lys Asp Gln Thr Ala
    295             300             305

aat ttg acc aat caa gga aaa aat att acc aaa aat gtg act ggt ttt     1074
Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys Asn Val Thr Gly Phe
310             315             320             325

ttc cag tct ttt aaa agc atc ctt act aat ccc ctg tat gtt atg ttt     1122
Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro Leu Tyr Val Met Phe
            330             335             340

gtg ctt ttg acg ttg tta caa gta agc agc tat att ggt gct ttt act     1170
Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr Ile Gly Ala Phe Thr
        345             350             355

tat gtc ttc aaa tac gta gag caa cag tat ggt cag cct tca tct aag     1218
Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly Gln Pro Ser Ser Lys
        360             365             370

gct aac atc tta ttg gga gtc ata acc ata cct att ttt gca agt gga     1266
Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro Ile Phe Ala Ser Gly
    375             380             385

atg ttt tta gga gga tat atc att aaa aaa ttc aaa ctg aac acc gtt     1314
Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe Lys Leu Asn Thr Val
390             395             400             405

gga att gcc aaa ttc tca tgt ttt act gct gtg atg tca ttg tcc ttt     1362
Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val Met Ser Leu Ser Phe
            410             415             420

tac cta tta tat ttt ttc ata ctc tgt gaa aac aaa tca gtt gcc gga     1410
Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn Lys Ser Val Ala Gly
            425             430             435

cta acc atg acc tat gat gga aat aat cca gtg aca tct cat aga gat     1458
Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val Thr Ser His Arg Asp
        440             445             450

gta cca ctt tct tat tgc aac tca gac tgc aat tgt gat gaa agt caa     1506
Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn Cys Asp Glu Ser Gln
    455             460             465

tgg gaa cca gtc tgt gga aac aat gga ata act tac atc tca ccc tgt     1554
Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr Tyr Ile Ser Pro Cys
470             475             480             485

cta gca ggt tgc aaa tct tca agt ggc aat aaa aag cct ata gtg ttt     1602
Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys Lys Pro Ile Val Phe
            490             495             500

tac aac tgc agt tgt ttg gaa gta act ggt ctc cag aac aga aat tac     1650
Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu Gln Asn Arg Asn Tyr
            505             510             515

tca gcc cat ttg ggt gaa tgc cca aga gat gat gct tgt aca agg aaa     1698
Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp Ala Cys Thr Arg Lys
```

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Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp Ala Cys Thr Arg Lys
        520                   525                   530

ttt tac ttt ttt gtt gca ata caa gtc ttg aat tta ttt ttc tct gca      1746
Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn Leu Phe Phe Ser Ala
        535                   540                   545

ctt gga ggc acc tca cat gtc atg ctg att gtt aaa att gtt caa cct      1794
Leu Gly Gly Thr Ser His Val Met Leu Ile Val Lys Ile Val Gln Pro
550                   555                   560                   565

gaa ttg aaa tca ctt gca ctg ggt ttc cac tca atg gtt ata cga gca      1842
Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser Met Val Ile Arg Ala
                570                   575                   580

cta gga gga att cta gct cca ata tat ttt ggg gct ctg att gat aca      1890
Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly Ala Leu Ile Asp Thr
                585                   590                   595

acg tgt ata aag tgg tcc acc aac aac tgt ggc aca cgt ggg tca tgt      1938
Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly Thr Arg Gly Ser Cys
        600                   605                   610

agg aca tat aat tcc aca tca ttt tca agg gtc tac ttg ggc ttg tct      1986
Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val Tyr Leu Gly Leu Ser
        615                   620                   625

tca atg tta aga gtc tca tca ctt gtt tta tat att ata tta att tat      2034
Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr Ile Ile Leu Ile Tyr
630                   635                   640                   645

gcc atg aag aaa aaa tat caa gag aaa gat atc aat gca tca gaa aat      2082
Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile Asn Ala Ser Glu Asn
                650                   655                   660

gga agt gtc atg gat gaa gca aac tta gaa tcc tta aat aaa aat aaa      2130
Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser Leu Asn Lys Asn Lys
                665                   670                   675

cat ttt gtc cct tct gct ggg gca gat agt gaa aca cat tgt              2172
His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu Thr His Cys
        680                   685                   690


taagggggaga aaaaaagcca cttctgcttc tgtgtttcca aacagcattg cattgattca      2232
gtaagatgtt attttttgagg agttcctggt cctttcacta agaatttcca catctttat      2292
ggtggaagta taaataagcc tatgaactta taataaaaca aactgtaggt agaaaaaatg      2352
agagtactca ttgtacatta tagctacata tttgtggtta aggttagact atatgatcca      2412
tacaaattaa agtgagagac atggttactg tgtaataaaa              2452

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Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
        35                  40                  45
Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
    50                  55                  60
Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
65                  70                  75                  80
Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
                85                  90                  95
Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
            100                 105                 110
Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
            115                 120                 125
Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
    130                 135                 140
Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
145                 150                 155                 160
Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
            165                 170                 175
Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
            180                 185                 190
Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr
            195                 200                 205
Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
    210                 215                 220
Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
225                 230                 235                 240
Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
            245                 250                 255
Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
            260                 265                 270
Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
            275                 280                 285
Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
            290                 295                 300
Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
305                 310                 315                 320
Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
                325                 330                 335
Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
            340                 345                 350
Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
            355                 360                 365
Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
    370                 375                 380
Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe
385                 390                 395                 400
Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val
                405                 410                 415
Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn
            420                 425                 430
Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
            435                 440                 445
Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
    450                 455                 460
Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
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465                     470                     475                     480
Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
                485                     490                     495
Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
            500                     505                     510
Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp
        515                     520                     525
Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn
    530                     535                     540
Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val
545                     550                     555                     560
Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser
                565                     570                     575
Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly
            580                     585                     590
Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly
        595                     600                     605
Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val
    610                     615                     620
Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr
625                     630                     635                     640
Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile
                645                     650                     655
Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser
            660                     665                     670
Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu
        675                     680                     685
Thr His Cys
        690
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<211> 1538
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<213> Homo sapiens

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gtctccaaac atgttgatgt gttttcaatg aaatggatgt ctgaggagaa aaccattagc     180
ctgagaaaac ccaaactgta ttcccattgt gaataaaagg aagtccataa aaatgatgga     240
aaatgttctg cattcctgtt atgatatcaa aatctggcag tacatgaaaa tttttcaaag     300
tgcttattta acaggcataa tctttggtct cctgagccag aatctgctgg gtatgggact     360
ggattgctat tttgacaact cgccagtaga ttcttactca gcagagtatt ggaagccttt     420
actctaatat tttggccttg ggtctacatt tctcagttct gcacagtcat tcttcccctc     480
tacactactc tttagtttgt ctcatgattc caatactctc aataattaac caagaataga     540
actaatcaat cagataactg tggcacagac atcaaataca ttttgctgca accatatcaa     600
caaatgtccc atgaatgata aggggtaacc atattctcat atatgcatcc tcacattacc     660
acatatatat atgtgcatat gtgtatacag gtaaaagtgt gtatatatgt atacatgtat     720
gtttgtgtgt atatacatac atatatcttc acacttttct gaaatatata tatttatgtg     780
agagaagggt ctgtacttta tttcagaaga gagcttaatg tccaaggtat aattgagagt     840
ctaaatgtt tgagttattg aattaattaa acttcatctc tactcaagaa aacttttaac     900
tgagttaagc tcttcctttc tccacaagtc aagtcaataa aaggaaactg tgatattaat     960
aattctttcc tgttttgatg taaagaatct atcgcataaa gcagtcttaa ttttcatcat    1020
tcagaaaaat ggtcttgcag ttaattggga ctctcttatt ccaggtggta tctccagtct    1080
ccatacatac cacgttagaa ccatacttat gtaccaagca aagagggtat attttaattt    1140
ttaaatgcca atgtaacctg taggcatatt ttttatttgt cttaaattat ttcctatttg    1200
gaagttttaa atacctggaa taatttattg tactcatatt tttaaagaaa aaaatcttat    1260
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gccaccaact taattgaata aacaagtaaa agccattccc aaaagtaagg tttacttgtt      1320
aagattaaca aaaaataatg tgagaattct gagaaatata atctttaaat attggcaact      1380
ggagtgaact cttaaaacta actaggtttt atatgtttga ctagagcaat gacataataa      1440
ggtggttaat catcactgga cttgttttca aaaagccaac tactttaaga ggaataaagg      1500
gtggacttgt tgcagttgct gtaggattct aaatccag                             1538
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<213> Homo sapiens

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gatactgcaa tggattgaag gtagaataag ttttatgttt ttgagctaaa ataagtaaat        60
agggaacttt aatgtataga aaagcaagtt gttaaaaaga acattatgtt tcaaattata       120
attttcaatt gaagcatata ttgaaatatt aacataatga ttcatacctt gatttaaacc       180
agtcttttaa tctgattaag                                                  200
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<210> 5
<211> 300
<212> DNA
<213> Homo sapiens

<400> 5
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tgacggaagc tttgaaattg gtaacattta ttttctattt taataaccaa acttgcaaag        60
ttaaaaaata tatatgcttt acaccactgg ttatcaactg gggtaaattt atctctcaca       120
ggcaatttgg caataactaa aaacatttgt ggttgtcata actgcacagg ggttgggggc       180
aatggaagtg ctactggtat ctaaaggtag aggtcagggg tactgctaaa tattctataa       240
tgcacaaaga atgatgtaac tgaaaatgtt gatagtgagg atgttcagaa accctgattc       300
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<210> 6
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<212> DNA
<213> Homo sapiens

<400> 6
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ccacatttct tcatgggata gtaagtgtta aaaaaaaaaa aaacctctgt gccactatca        60
gtaccttgta aattaggagt agaattttat tattatccct ttaaataggc agttacccttt      120
tgagaagata cccactaagt gtgtacagaa atgaaatagt gtctatttgt ctacataatc       180
attttattta tcgtagcttt catatacttt gaaataacaa aaagactaaa ctgtagagtt       240
tcaaatgaaa taaataggct ttttatgaat ttttagtata acgtatatac tgtacgtctt       300
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<210> 7
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<212> DNA
<213> Homo sapiens

<400> 7
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acctgagata gtgggaaaag gtaagaatta atattgacag taaaaagtct tctaaaatgt        60
atacatttaa ttacatctct aaaaattgtt gtgatattca ttagcaaaat ttaattaaga       120
atgaatagga aaaacatttg actcttacag acataattat agtgttaata tacacagttc       180
gcccattaac aacacaggtt taaactacgc gttttcactt ctatgcaaat tttgtccatc       240
tgaactggat gataaacctg ccggtaagaa tatctgacat tttctatatt tggattgaac       300
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<210> 8
<211> 200
<212> DNA
<213> Homo sapiens

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<400> 8
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tacttgtact tgtaaattaa aaaaaaataa gtagaataat taagagttta caagtagtta   120
aatttgtaat agaaatgcta aaattaatgt ttaaaatgaa acactctctt atctacatag   180
gttgtttaaa ggaatctggg                                               200

<210> 9
<211> 200
<212> DNA
<213> Homo sapiens

<400> 9
tattggatat gtagatctaa gtaagtacaa ccagaacaag gtaccatgat aacgtctttc    60
taagcacaca tgcgaaaaac attttttcaa ataactgaat tcactctttc aatagtcctt   120
tgcttaatat aattagaaag ttacaagtag gaaataaatg tattactaat cagaataaat   180
ataaaatcca gctcctattt                                               200

<210> 10
<211> 203
<212> DNA
<213> Homo sapiens

<400> 10
ttaaaaaaaa ctttgccatt tcgtcatcat caaagcaaat ttcttcatat aaagaaaaat    60
tctttatcta cttttttttt tccctctttc tctgctttca ctttacttct tccttctcct   120
ccccttcttt gtcttttct tctctctctc tcttttgat atatgtctat catatatttc     180
cagaaataat ccagtgacat ctc                                           203

<210> 11
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<212> DNA
<213> Homo sapiens

<400> 11
catgtcatgc tgattgttaa gtaagtatga cttttaaaaa cattttcata tgcatgagac    60
tataaacaca cctaatgata tgcatatttt tacataatat actgggaatt caaattcata   120
tttcatcaaa ttttaatttt ctgagaattc attttattaa aatttactat gaactctcaa   180
ggctgtaatt aataattttg c                                             201

<210> 12
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<212> DNA
<213> Homo sapiens

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tgatttgggt ctttgagatt tctaataatc tttattattg ggtagatgca gaacaaaata    60
ataaacgaat cctccaaatt tttgaacttt tatttaatca aaatatatca atgtggaata   120
tcatgcagtt acatttaaaa tatgttccct aaactgacat cttctcttct cctattacag   180
gaggaattct agctccaata                                               200
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